

OM ref. 03-09-025 998A 1 ft. Swiss 2001 39 + 11" front 162

Date: Apr 23, 2002 10:41 PM

About: Results were produced by the GenCore software, version 4.5.  
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Command line parameters:

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MODEL-frame=22p.model -DEV xlp
-O -c 0.001 -S 0.001 -SPR 0.001 -GAPF 0.001 -VACV 0.001 -APP_query fastx_align
-DB-SwissProt_39 -QMT-lastan -SUFFIX-fsp -GAPOP=12.000
-CAPXIT=4.000 -MINMATCH=0.100 -LCPH=1.0 0.000 -LCPH-X1=0.000
-QCAPXIT=4.500 -CGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX-blcsmsv2
TRANS-human40.cdi -LIST=45 -LOCALIGN=200 -THR_SCORE=pct.
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTEMT=pls
-NORM-OXT -MINLEN=0 -MAXLEN=2000000000
-USER-US09525348.acGN1_1.43 -NCPU=6 -LCPH=3 -LONGLOG -NO_XIPXY
-WAIT -THREADS=1
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Search information block:

Query: US-09 525 998A 1

Query length: 1368

Query length: 1366  
Database: Swissprot 39.4\*

Database: swissprot\_39; Database sequences 100059

Database sequences: 100079  
Database length: 36664837

Database length: 36664827  
Search time (sec): 87.870000

score_list:	Seq	Strd	Orig	ZScore	EScore	Len	Documentation
Sequence							
SwissProt_39-TNR1_HUMAN	+ 2487.00	2514.76	4.6e-133	455	p19438 homo sapiens (human)		
SwissProt_39-TNR1_PIG	+ 1748.00	1592.68	3.0e-91	461	P05055 swa serofa (pig) tumor		
SwissProt_39-TNR1_RAT	+ 1642.00	1578.55	3.0e-91	461	P05044 rattus norvegicus (rat)		
SwissProt_39-TNR1_MOUSE	+ 1521.00	1539.77	9.5e-79	454	P25118 mus musculus (mouse)		
SwissProt_39-TNR1_BOVIN	+ 1517.00	1535.46	1.6e-78	471	O16131 bos taurus (bovine)		
SwissProt_39-MST1_HUMAN	+ 374.00	382.69	2.9e-14	417	P09303B hws1-l protein precu		
SwissProt_39-TNRC_HUMAN	+ 249.00	297.60	1.5e-00	435	P16941 homo sapiens (human)		
SwissProt_39-NRGP_HUMAN	+ 240.00	247.77	9.3e-07	427	P169138 homo sapiens (human)		
SwissProt_39-TNCP_MOUSE	+ 224.00	231.83	7.4e-06	415	P05284 mus musculus (mouse)		
SwissProt_39-NRFP_RAT	+ 223.00	230.14	8.9e-06	425	M07174 rattus norvegicus (rat)		
SwissProt_39-INP2_MOUSE	+ 205.00	211.17	9.1e-05	474	P25119 mus musculus (mouse)		
SwissProt_39-TN2_HUMAN	+ 204.00	210.37	0.0001	461	P25133 homo sapiens (human)		
SwissProt_39-VT2_MXVL	+ 200.00	208.87	0.0002	426	P25455 myxoma virus (strain 1		
SwissProt_39-NRFP_CHICK	+ 187.50	204.56	0.0002	416	P19510 gallus gallus (chicken		
SwissProt_39-VT2_SVKA	+ 192.00	200.82	0.0005	325	P25043 Shope fibrocyte virus (S		
SwissProt_39-FASA_MOUSE	+ 191.00	199.65	0.0006	327	M07746 swa serofa (pig) fast		
SwissProt_39-FASA_PIG	+ 179.00	189.08	0.0027	269	P09203 bos taurus (bovine)		
SwissProt_39-CD40_BOVIN	+ 177.00	185.70	0.0035	324	Q63390 rattus norvegicus (rat)		
SwissProt_39-FASA_RAT	+ 177.00	185.46	0.0035	335	P25445 homo sapiens (human)		
SwissProt_39-CIM4O_MOUSE	+ 176.50	185.63	0.0038	289	P25752 mus musculus (mouse)		
SwissProt_39-AU08_HUMAN	+ 176.00	177.95	0.0038	824	P19325 homo sapiens (human)		
SwissProt_39-AU08_BOVIN	+ 175.50	184.21	0.0043	824	P25387 bos taurus (bovine)		
SwissProt_39-VG16_HSV2II	+ 168.50	171.49	0.0100	629	P14290 herpes simplex virus		
SwissProt_39-ISSPO_BOVIN	+ 168.50	169.91	0.0099	867	P198157 bos taurus (bovine)		
SwissProt_39-CD40_HUMAN	+ 166.50	176.25	0.0138	277	P25742 homo sapiens (human)		
SwissProt_39-CD32_HUMAN	+ 166.00	176.21	0.0147	260	P126812 homo sapiens (human)		
SwissProt_39-VC22_VAPV	+ 164.00	173.04	0.0189	349	P13015 variola virus (protein		
SwissProt_39-C030_HUMAN	+ 156.00	163.08	0.0347	595	P294908 homo sapiens (human)		
SwissProt_39-YHLLI_EBV	+ 157.00	160.50	0.0447	560	P09391 Epstein-Barr virus (str		
SwissProt_39-TN1C4_MOUSE	+ 156.50	151.80	0.0447	1964	P13695 mus musculus (mouse)		
SwissProt_39-VG3P_EBAVB	+ 156.00	157.13	0.0500	886	P07284 Epstein-Barr virus (S		
SwissProt_39-HMFI_HUMAN	+ 145.50	162.49	0.0560	392	P05925 homo sapiens (human)		
SwissProt_39-SMNC_RAT	+ 155.50	155.04	0.0541	900	Q6WJ13 rattus norvegicus (rat)		
SwissProt_39-IR14_HUMAN	+ 155.00	164.49	0.0609	283	P092956 homo sapiens (human)		
SwissProt_39-P058_HUMAN	+ 154.50	158.18	0.0620	625	O14202 homo sapiens (human)		
SwissProt_39-VS41-ITALA	+ 153.50	156.47	0.0701	687	P19127 glandia lambda (Glari		
SwissProt_39-GRN_CAVPO +	152.50	156.57	0.0805	591	P28767 cavida porcellus (guine		
SwissProt_39-VG3P_PHV	+ 152.50	153.43	0.0785	907	P03200 Epstein-Barr virus (str		
SwissProt_39-MY15_HUMAN	+ 152.50	143.47	0.0724	3530	P09087 homo sapiens (human)		































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343 hrGlyGlySerValThrValThrGlyAsnThrIleTyrAsnGlyHis 359
953 ATCAAGAGGAGTGAAC.....ACATAGATTCAGACACAGGAGCTGAGAC 996
360 ValLeuGlyGlyThrArgGlyProGly AspProProAlaIleProGly 375
997 CCCATCC.....CCAGCCGCCICAGAAATTCAGACACAGGAGCTGAGAC 1043
375 uProProTyrProThrPro GlyGlyGlyAlaProGlyProSerGlu 390
1044 ACACAGGCTCACACATACACACCCG 1069
391 .....LeuSerThrPro 394
seq_name: SwissProt_49:NGFR_RAT
seq_documentation_block:
ID NGFR_RAT STANFORD: PRT: 425 AA.
AC P07174:
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 20-AUG-2001 (Rel. 43, Last annotation update)
DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
DE (GP80-NGFR) (P75 ICD).
DE NGFR.
OS Rattus norvegicus (Rat.).
OC Eukaryota; Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCHI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=87115859; PubMed=3027580;
RA Radeke M.J., Misko T.P., Iisu C., Herzenberg L.A., Shooter E.M.;
RT "Gene transfer and molecular cloning of the rat nerve growth factor
RT receptor."
RL Nature 325:593-597(1987).
RN [2]
SEQUENCE OF 1-22 FROM N.A.
RX TISSUE=Liver;
RX MEDLINE=93077038; PubMed=1446821;
RA Metcalf M., Timmusk T., Allikmets P., Saarman M., Persson H.;
RT "Regulatory elements and transcriptional regulation by testosterone
RT and retinoic acid of the rat nerve growth factor receptor precursor."
RL Gene 121:247-254(1992).
RN [3]
STRUCTURE BY NMR OF 334-419.
RX MEDLINE=97449145; PubMed=9305641;
RA Liepinsh E., Ilag L.L., Otting G., Ibanes C.F.;
RT "NMR structure of the death domain of the p75 neurotrophin receptor."
RL EMBO J. 16:4999-5005(1997).
CC [1] FUNCTION: LOW AFFINITY PEPTIDE WHICH CAN BIND TO NGF, BDNF,
CC NT-3, AND NT-4.
CC [2] SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
CC BOND FORMATION.
CC [3] SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC [4] PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
CC [5] SIMILARITY: CONTAINS A LA-NGF/TNFR-TYPE CYSTEINE-RICH REGION.
CC [6] SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as this content is in no way
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CC or send an email to license@sib-sib.ch)
CC
CC EMBL: X05137; CAA28783.1.
CC EMBL: X61269; NOT_ANNOTATED_CDS.
CC PIR: A26431; A26431.
CC DOI: 1NGR; 29-JUL-97.
CC InterPro: IPR000448; death
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00531; death_1.
DR Pfam: PF00020; TNFR_c6; 4.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS00650; TNFR_NGFR_2; 4.
DR PROSITE: PS0017; DEATH_DOMAIN; 1.
KW Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
KW Phosphorylation; Signal; 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 425 LOW AFFINITY NERVE GROWTH FACTOR
FT RECEPTOR.
FT DOMAIN 30 251 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 252 273 POTENTIAL.
FT DOMAIN 274 425 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 32 190 4 X TNFR-CYS.
FT REPEAT 32 66 TNFR-CYS 1.
FT REPEAT 67 108 TNFR-CYS 2.
FT REPEAT 109 148 TNFR-CYS 3.
FT REPEAT 149 190 TNFR-CYS 4.
FT DOMAIN 198 249 SER/THR-RICH.
FT DOMAIN 354 419 DEATH.
FT DISULFID 33 44 BY SIMILARITY.
FT DISULFID 45 58 BY SIMILARITY.
FT DISULFID 48 65 BY SIMILARITY.
FT DISULFID 68 84 BY SIMILARITY.
FT DISULFID 87 100 BY SIMILARITY.
FT DISULFID 90 108 BY SIMILARITY.
FT DISULFID 110 123 BY SIMILARITY.
FT DISULFID 126 139 BY SIMILARITY.
FT DISULFID 129 147 BY SIMILARITY.
FT DISULFID 150 165 BY SIMILARITY.
FT DISULFID 168 181 BY SIMILARITY.
FT DISULFID 171 189 BY SIMILARITY.
FT CARBOHYD 61 61 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 71 71 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SOURCE 425 AA; 45432 MW; R2E15293D3827F8 CRC64,
alignment_scores:
Query: 425.00 Length: 495
Ratio: 1.057 Gaps: 27
Percent Similarity: 42.626 Percent Identity: 23.232
alignment_block:
US-09-525-998A-1 x NGFR_RAT
Align seq 1/1 LO: NGFR_RAT from: 1 to: 425
40 GTAATTTGAGACTTTGTTGGGAATATACCCCTCAGGGGTTATTGGACT 89
16 LeuLeuLeuLeuLeuLeuValSerSerGlyGlyAla..... 29
90 GCGCTCTCATTAGGGGACAGGACAGACAGACAGACAGACAGACAGACAG 139
30 ..... 1
140 GAAATATATATACCTTAAATAATTCGATTGCTHATCAAGTGCAC 189
36 LysLeuThrCysSerThrG 36
190 AAGAGAAATTTATTTATTAATATATGTTTAAAGGAGGAGGAGGAGGAG 239
50 LeuGlyGlyGlyAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 64
240 CAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 286
64 LysGluProCysLeuAspAsnValThrPheSerAspValValSerAlaAla 81
287 TCAGACACTGCTCAGACTCAGACTCAGACTCAGACTCAGACTCAGACTG 436
81 ArgGlyProCysLeuSerThrGlyGlyGlyGlyGlyGlyGlyGlyGly 94

```





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```

CC -----
CC
CC
CC
CC
DR EMBL: M60469: AAA39752.1: -
DR EMBL: M59378: AAA0463.1: -
DR EMBL: U39488: AAA85021.1: -
DR EMBL: X87128: CAA60618.1: -
DR PUR: H38634: H38634.
DR HSSP: P19438: INCF.
DR MGI: 131484: Infrsflb
DR InterPro: IPR001368: TNFR_c6.
DR Pfam: PF00202: TNFR_c6: 4.
DR ProDom: PD000771: TNFR_c6: 1.
DR SMART: SM00208: TNFR_4.
DR PROSITE: PS00652: TNFR_NCFR_1: 2.
DR PROSITE: PS00650: TNFR_NCFR_2: 3.
KW Receptor. Transmembrane; Glycoprotein; Repeats; Signal.
FT SIGNAL 1 22
FT CHAIN 23 474
FT DOMAIN 23 268
FT TRANSMEM 259 288
FT DOMAIN 289 474
FT DOMAIN 39 203
FT REPEAT 39 77
FT REPEAT 78 119
FT REPEAT 120 164
FT REPEAT 165 203
FT DISULFID 40 54
FT DISULFID 55 68
FT DISULFID 58 76
FT DISULFID 79 94
FT DISULFID 97 111
FT DISULFID 101 119
FT DISULFID 121 127
FT DISULFID 136 145
FT DISULFID 139 163
FT DISULFID 166 181
FT CARBOHYD 69 69
FT CARBOHYD 195 195
SQ SEQUENCE 474 AA: 50319 MW: 46284398406563 CMC64;

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## alignment\_scores:

Quality: 205.00 Length: 254  
Ratio: 1.614 Gaps: 11  
Percent Similarity: 50.000 Percent Identity: 26.378

## alignment\_block:

US-09-525-998a-1 x TNR2\_MOUSE

Align seq 1/1 to TNR2\_MOUSE from 1 to 474

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130 TGTCTCTAAAGAAATAATATCTAATCTCAAAATATATATATCTAT* 179
|||||
40 CysGlnTleSerGlnGlnTyrTyrAspAsqLysAlaGlnMetCysCysAl 56
180 CAAGIGTCATCAAGCAAGCTACTCTGATCAATATGATCTGCTCCAGCCGCGCG 229
|||||
56 aLysCysProFroGlnTyrValIleGlnHisPheCys...AsnLysThrS 72
240 AGATATATATCTCAATATATCTGATGATGATCTCTCTCTCTCTCTCTCAAA 279
|||||
72 crAspGlnValCysAlaLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 88
280 AACCACTCTCAAGCAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 326
|||||
89 AsnGlnPheArgThrCysLeuSerCysSerSerSerSerSerSerSerSer 104
327 GGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 376
105 ....GlnValGlnIleArgArgArgArgArgArgArgArgArgArgArgArg 120

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377 GGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 414
|||||
120 laCysGlnAlaGlyArgTyrCysAlaLeuIysThrHis.....SerGly 134
|||||
415 AACCTTTTCCAGTCCTTCAATTCATTCAGCCCTCTGCTGCTGCTGCTGCT 461
|||||
135 SerCysArgGlnCysMetArgLeuSerLysCysGlyFroGlyPheGlyVa 151
|||||
462 CCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 508
|||||
151 laLaserSerArgAlaProAsnGlyAsnValLeuCysLysAlaCysAlaP 168
|||||
509 CAGCTTTTCTTAAAGAAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 558
|||||
168 laGlyThrPhe.....SerAspFluThrSerThrAspValCysArg 182
|||||
559 AAAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 608
|||||
183 ProIleArgIleCysSerIleLeuAlaIleProGlyAsnAlaSerThrAs 199
|||||
609 GGGT.....ACACAGCACTCAGGACACAGAGCTGCTGCTGCTGCTGCT 652
|||||
199 paLysValCysAlaProGlnSerProThrLeuSerAlaIleCProArgThr 216
|||||
653 TTTCTTGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 702
|||||
216 enyVal..... 218
703 CCGACCAACCGCTGCAAGCTCAGAGCTCTCTCTCTCTCTCTCTCTCTCT 752
|||||
219 ..... 219
753 GAGAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 802
|||||
219 rGlnProGlnPro.....ThrArgSerGlnProGln 230
803 CCGTAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 852
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230 spGlnGlnProGlyProSerClnThrProSerIleLeuThrSerLeuGly 246
853 TTCAGTCCCGCTG 864
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247 SerThrProIle 250

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seq\_name: SwissProt\_39.TNR2\_HUMAN

seq\_documentation\_block:

ID TNR2\_HUMAN STANDARD; PRT; 461 AA.  
AC P20333;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-AUG-1991 (Rel. 19, last sequence update)  
DT 28-AUG-2001 (Rel. 40, last annotation update)  
DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR  
DE BINDING PROTEIN 2) (TNF1) (P80) (TNF-R2) (F75) (CD120B) (ETANERCEPT).  
GN TNFRSF1B OR TNFR2 OR TNFR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catartida; Homidae; Hominidae.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90260639; PubMed 2160731;  
RA Smith G.A., Davis T., Anderson D., Solam L., Heckmann M.P., Jerry R.,  
RA Power S.K., Cosman D., Goodwin R.G.;  
RT "A receptor for tumor necrosis factor defines an unusual family of  
cellular and viral proteins";  
PL Science 248:1019-1024(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91045991; PubMed-2172983;  
RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,  
RA Hale K.K., Squires C.H., Thompson P.G., Vannice J.L.;  
RT "A second tumor necrosis factor receptor gene product can shed a







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FT DOMAIN 188 246 SEP/TUP-PICH
FT DOMAIN 333 410 DEATH
FT DISULFID 24 35 HY SIMILARITY.
FT DISULFID 36 49 HY SIMILARITY.
FT DISULFID 39 56 HY SIMILARITY.
FT DISULFID 59 75 HY SIMILARITY.
FT DISULFID 78 91 HY SIMILARITY.
FT DISULFID 81 99 HY SIMILARITY.
FT DISULFID 101 114 HY SIMILARITY.
FT DISULFID 117 130 HY SIMILARITY.
FT DISULFID 120 138 HY SIMILARITY.
FT DISULFID 141 156 HY SIMILARITY.
FT DISULFID 159 172 HY SIMILARITY.
FT DISULFID 162 180 HY SIMILARITY.
FT CARBOHYD 52 52 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 36 36 C -> Y (IN REF. 2).
FT CONFLICT 173 173 F -> K (IN REF. 2).
FT CONFLICT 276 276 N -> S (IN REF. 2).
FT CONFLICT 396 396 K -> R (IN REF. 2).
SQ SEQUENCE 416 AA: 44654 MW: 60624 MB54F4D256 GRG64.

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## alignment\_scores:

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Quality: 197.50 Length: 489
Ratio: 0.890 Gaps: 32
Percent Similarity: 45.09 Percent Identity: 23.92%

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## alignment\_block:

US-09-525-998a-1 x NGPR\_CHECK

Align seq 1/1 to: NGPR\_CHECK from: 1 to: 416

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31 CIGCCACGCGCTCCCTCCAGCTGCTGGTGGGATAATACCCGACAGGGT 80
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
5 ValProteinLeuLeu.....LeuLeuProAlaGly.. 15

81 TATTGATGCTGCTCTACTATAGAGACAGAGAAAGAAATATGTGT 130
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
16 ProthyrpGlySerThrCysLeu.....C 24

131 GPCGCCAAGAAATATATACCCGCTCAAAATATTCGATTGCTGTAQC 180
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
24 ysLeuThrLysMetLys.....ThrThrSerGlyGluCysCysLys 37

181 AAGTCCCAACAAGCACTACTTGTACAAATACGTCGACGCGCCGCGCA 230
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
38 AlaCysAsnLeuGlyGluGlyValValClnProCys...GlyValAsnG 53

241 GATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 277
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
53 n.....ThrValCysGluProCysLeuAspSerValThrIysSerAspThrV 69

278 AAACACACCTCACACACTGCTCCACCTCCCTCCAAATGCCAAGAGAAATG 327
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
69 alSerAlaThrGluProCysLysProCysThrGlyCys.....Val 82

328 GGTACAGGACGACGACGACGACGACGACGACGACGACGACGACGAC 374
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
83 GlyLeuHisSerMetSerAlaProCysValClnSerAspAlaValC 99

375 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 424
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
99 sArgCys.....AlaIysGlyIysThrGlnAspGluLeuSerCys 113

425 ACTGCTGCAATTCAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 471
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
113 erCysLysGluCysSerIleCysClnValGlyThrGlyLeuMetPhePro 159

472 TCCACCAACAACAACAACAACAACAACAACAACAACAACAACAACA 518
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
130 CysArgAspSerGlnAspThrValCysGluCysProGluGlyThrPh 146

519 TCTAAGAA.....AAGAGTGTGTCTCTGTGTGTGTGTGTGTGT 556

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146 eSerAspGluAlaAsnPheValAspProCysLeuProCysThrIleCysG 163
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
557 AGAAAGCCGCGACGACGACGACGACGACGACGACGACGACGACGACG 606
   .. ||||| ||||| ||||| ||||| ||||| ||||| |||||
163 LuGluAsnGluValMetValLysGluCys..... 172

607 AAGGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 656
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
173 ThrAlaThrSerAspAlaGluCysArgAspLeuHisPro..... 185

657 CTITGATCTTGATCTTGATCTTGATCTTGATCTTGATCTTGATCTTGAT 706
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
185 .. 185

707 ACTAAGGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTGCAAG 756
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
186 AtqTrpThrThrHisThrProSerLeu AlaGlySerAspSer 199

757 CCTGAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 806
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
200 ProGlu.....ProIleProTat 205

807 AAAATATATATATATATATATATATATATATATATATATATATATAT 856
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
206 qAspPro...PheAsn...ThrGluGlyMetAlaThrThrLeu AlaAsp 219

857 GTCCCGCTCC.....CCAGTCCACCTTCACCTCC 885
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
220 IleValThrThrValMetGlySerSerGlnProValValSerArgGlyTh 236

886 AATCTATATATATATATATATATATATATATATATATATATATATAT 925
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
236 rAlaAspAsnLeuIleProValIysCysSerIleClnAlaValValValV 253

926 ..CTCTCTGATATATATATATATATATATATATATATATATATATATAT 958
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
253 alGlyLeuValAlaIleAlaPheLysArgTrpAsnSerCysLysGln 269

959 GAGTGTACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1008
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
270 AsnLysGlnGlyAlaAsnAsnArgProValAsnGlnThrProSerProGl 286

1009 CCGTTTCAGA.....ACTGACAG GATAGCG 1033
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
286 cGlyGlyLysLeuHisSerAspSerGlyIleSerValAspSerGlnSerL 403

1034 GGTAT.....AAGATATATATATATATATATATATATATATATATATAT 1071
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
303 euHisAspGlnGlnProProAsnGlnSerThrGlnGlyProAlaProLys 419

1072 ..ACGCTACGCGCTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1110
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
320 GlyAspGlySerLeuTyrAla.....SerLeuProSerLysGln 333

1111 .....TGGAAGG 1117
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
333 nGluGluValGluLysLeuLeuSerSerAlaGluGluThrTrpArgG 350

1118 AATTGCTGCGCGCTAGGGCTAGGGCTAGGGCTAGGGCTAGGGCTAGGGCT 1167
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
350 lnLeuAlaGlyGluLeuGlyTyrIysGlnAspLeuLeuAsp..... 363

1168 CTGCGAAGCGGGGCTGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1208
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
364 .....CysPheThrArgGluGluSerProAlaArgAlaLe 375

1209 GCTATATATATATATATATATATATATATATATATATATATATATAT 1258
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
375 uGluAlaAspTrp.....SerAlaLysGluThrAlaThrLeuAspA 489

1259 TGCTGGAGAGGCTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1308
   ||||| ||||| ||||| ||||| ||||| ||||| |||||

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816 CTTCAAGTCCCACTCAAGCTTCACACCAAGCTGGGCTTCAGT..... 858
      |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
193 uV41111etysThryscLeupheThrValThrLeuAsnTyThrAspCysA 210

859 ...CAGGTGCCAAGTCCCACTTCACACCAAGCTCC 891
      |||||  |||  |||  |||||  |||
210 sProValPheHisThrGluTyrTyrAlaThrSer 221

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